



wwPDB EM Validation Summary Report ⓘ

Nov 7, 2022 – 02:47 PM JST

PDB ID : 5X8R
EMDB ID : EMD-6710
Title : Structure of the 30S small subunit of chloroplast ribosome from spinach
Authors : Ahmed, T.; Shi, J.; Bhushan, S.
Deposited on : 2017-03-03
Resolution : 3.70 Å(reported)

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We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

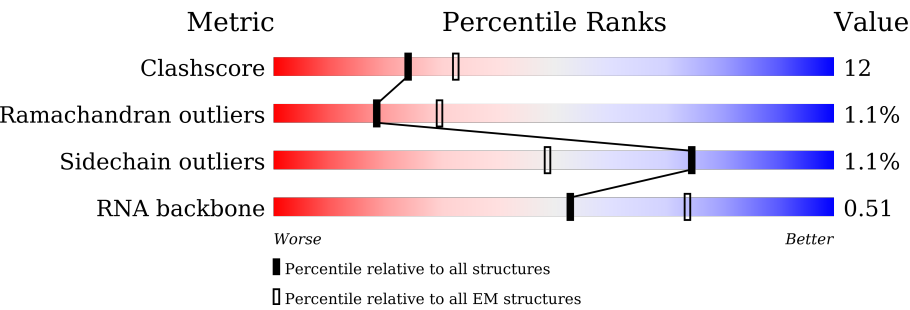
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	b	236	<div><div>63%</div><div>91%</div><div></div><div></div><div></div><div></div><div></div></div>
2	c	218	<div><div>13%</div><div>95%</div><div></div><div></div><div></div><div></div><div></div></div>
3	e	253	<div><div>6%</div><div>65%</div><div></div><div></div><div></div><div></div><div>32%</div></div>
4	f	146	<div><div>21%</div><div>75%</div><div></div><div></div><div></div><div></div><div>24%</div></div>
5	g	155	<div><div>26%</div><div>95%</div><div></div><div></div><div></div><div></div><div></div></div>
6	h	134	<div><div>10%</div><div>99%</div><div></div><div></div><div></div><div></div><div></div></div>
7	i	157	<div><div></div><div>82%</div><div></div><div></div><div></div><div></div><div>15%</div></div>

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Mol	Chain	Length	Quality of chain
8	j	122	
9	k	138	
10	l	123	
11	m	126	
12	o	90	
13	p	88	
14	q	108	
15	r	101	
16	s	92	
17	t	108	
18	u	137	
19	y	236	
20	a	1491	
21	w	121	
22	d	201	
23	v	198	
24	n	100	
25	x	47	
26	8	370	

2 Entry composition

There are 26 unique types of molecules in this entry. The entry contains 55412 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 30S ribosomal protein S2, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	b	227	Total	C	N	O	S	0	0
			1787	1127	326	321	13		

- Molecule 2 is a protein called 30S ribosomal protein S3, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	c	213	Total	C	N	O	S	0	0
			1719	1099	310	304	6		

- Molecule 3 is a protein called 30S ribosomal protein S5, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	e	171	Total	C	N	O	S	0	0
			1292	806	250	230	6		

- Molecule 4 is a protein called 30S ribosomal protein S6 alpha, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	f	111	Total	C	N	O	S	0	0
			886	566	145	171	4		

- Molecule 5 is a protein called 30S ribosomal protein S7, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	g	149	Total	C	N	O	S	0	0
			1161	723	231	204	3		

- Molecule 6 is a protein called 30S ribosomal protein S8, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	h	134	Total	C	N	O	S	0	0
			1088	684	211	187	6		

- Molecule 7 is a protein called 30S ribosomal protein S9, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	i	133	Total	C	N	O	S	0	0
			1020	650	191	178	1		

- Molecule 8 is a protein called protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	j	98	Total	C	N	O	S	0	0
			796	512	142	137	5		

- Molecule 9 is a protein called 30S ribosomal protein S11, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	k	118	Total	C	N	O	S	0	0
			887	549	182	151	5		

- Molecule 10 is a protein called 30S ribosomal protein S12, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	l	123	Total	C	N	O	S	0	0
			967	604	198	162	3		

- Molecule 11 is a protein called 30S ribosomal protein S13, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	m	110	Total	C	N	O	S	0	0
			898	559	183	153	3		

- Molecule 12 is a protein called 30S ribosomal protein S15, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	o	62	Total	C	N	O	S	0	0
			525	339	100	85	1		

- Molecule 13 is a protein called 30S ribosomal protein S16, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	p	80	Total	C	N	O	S	0	0
			664	425	123	114	2		

- Molecule 14 is a protein called protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	q	78	Total	C	N	O	S	0	0
			635	399	124	108	4		

- Molecule 15 is a protein called 30S ribosomal protein S18, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	r	64	Total	C	N	O	S	0	0
			518	326	101	90	1		

- Molecule 16 is a protein called 30S ribosomal protein S19 alpha, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	s	78	Total	C	N	O	S	0	0
			627	403	118	104	2		

- Molecule 17 is a protein called protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	t	105	Total	C	N	O	S	0	0
			832	514	169	148	1		

- Molecule 18 is a protein called protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	u	44	Total	C	N	O	S	0	0
			393	238	87	66	2		

- Molecule 19 is a protein called protein plastid pY.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	y	108	Total	C	N	O	S	0	0
			845	521	164	159	1		

- Molecule 20 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	a	1480	Total	C	N	O	P	0	0
			31777	14168	5863	10266	1480		

- Molecule 21 is a protein called protein cS23.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	w	84	Total	C	N	O	S	0	0
			689	454	115	118	2		

- Molecule 22 is a protein called 30S ribosomal protein S4, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	d	199	Total	C	N	O	S	0	0
			1633	1032	319	278	4		

- Molecule 23 is a protein called protein cS22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	v	190	Total	C	N	O	S	0	0
			1464	908	255	298	3		

- Molecule 24 is a protein called 30S ribosomal protein S14, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	n	99	Total	C	N	O	S	0	0
			819	507	174	135	3		

- Molecule 25 is a protein called protein bTHXc.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	x	37	Total	C	N	O	0	0
			289	179	65	45		

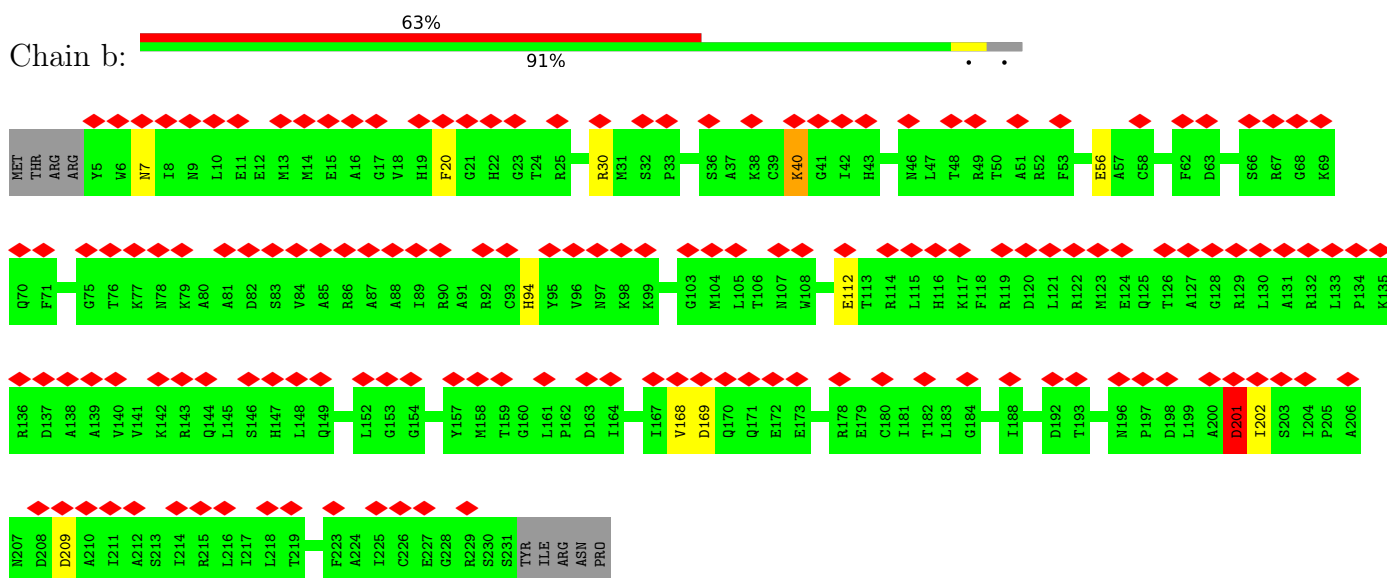
- Molecule 26 is a protein called 30S ribosomal protein S1, chloroplastic.

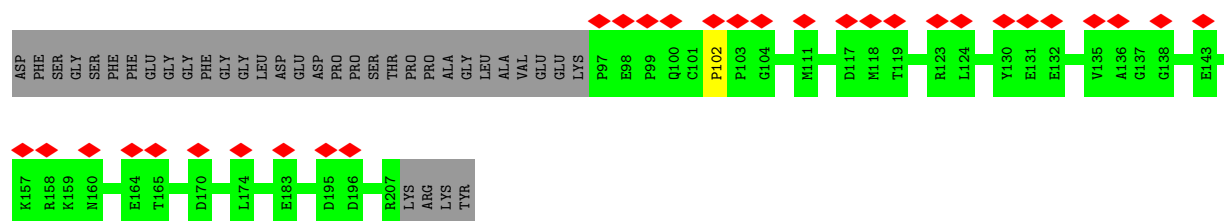
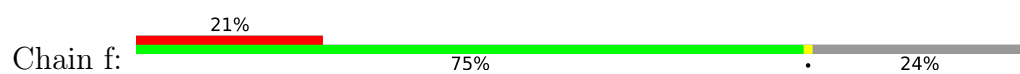
Mol	Chain	Residues	Atoms					AltConf	Trace
26	8	154	Total	C	N	O	S	0	0
			1201	744	222	227	8		

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: 30S ribosomal protein S2, chloroplastic

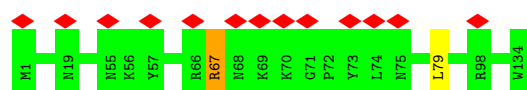




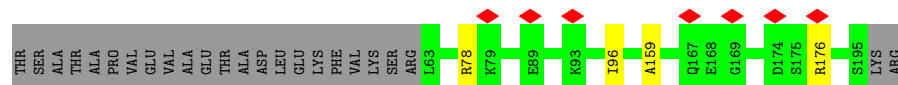
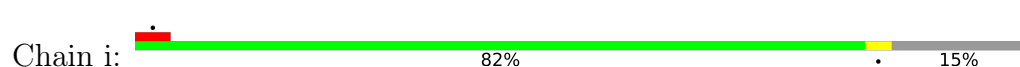
- Molecule 5: 30S ribosomal protein S7, chloroplastic



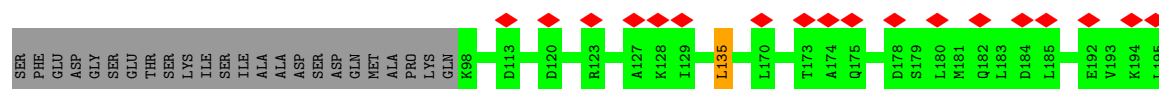
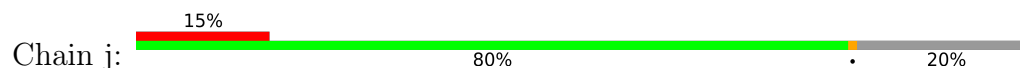
- Molecule 6: 30S ribosomal protein S8, chloroplastic



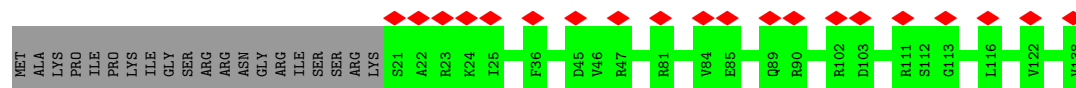
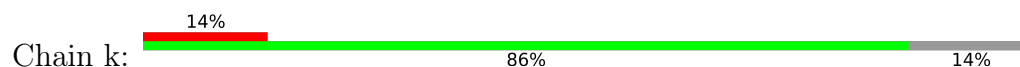
- Molecule 7: 30S ribosomal protein S9, chloroplastic



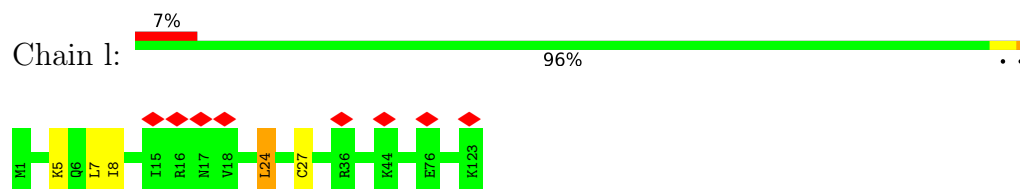
- Molecule 8: protein S10



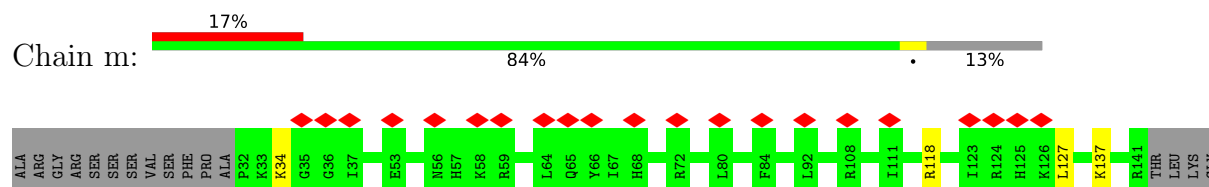
- Molecule 9: 30S ribosomal protein S11, chloroplastic



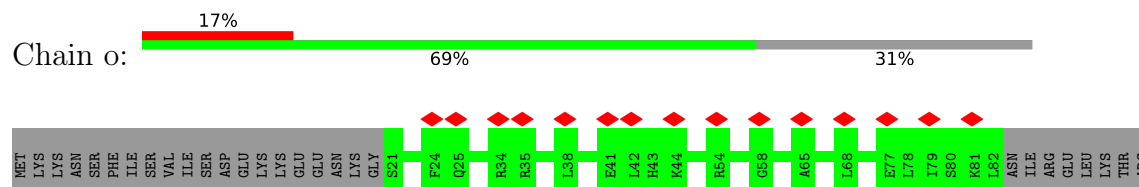
- Molecule 10: 30S ribosomal protein S12, chloroplastic



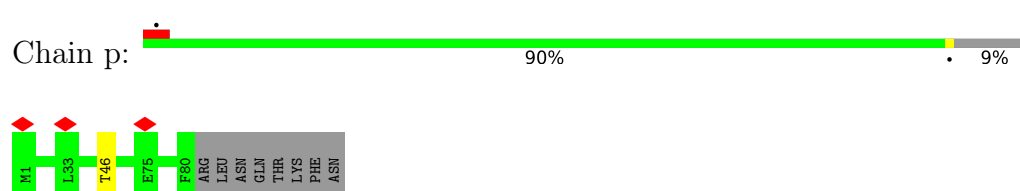
- Molecule 11: 30S ribosomal protein S13, chloroplastic



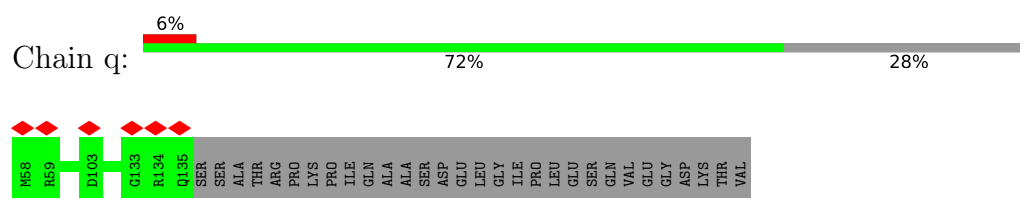
- Molecule 12: 30S ribosomal protein S15, chloroplastic



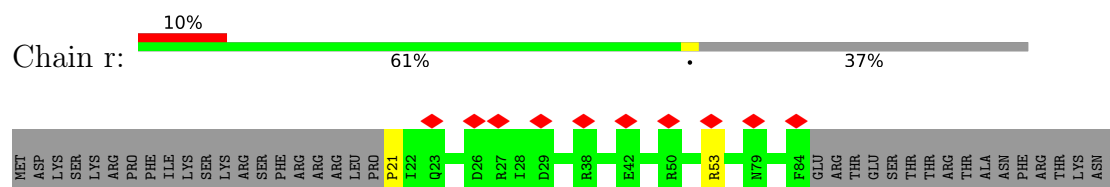
- Molecule 13: 30S ribosomal protein S16, chloroplastic



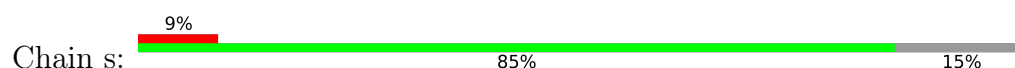
- Molecule 14: protein S17

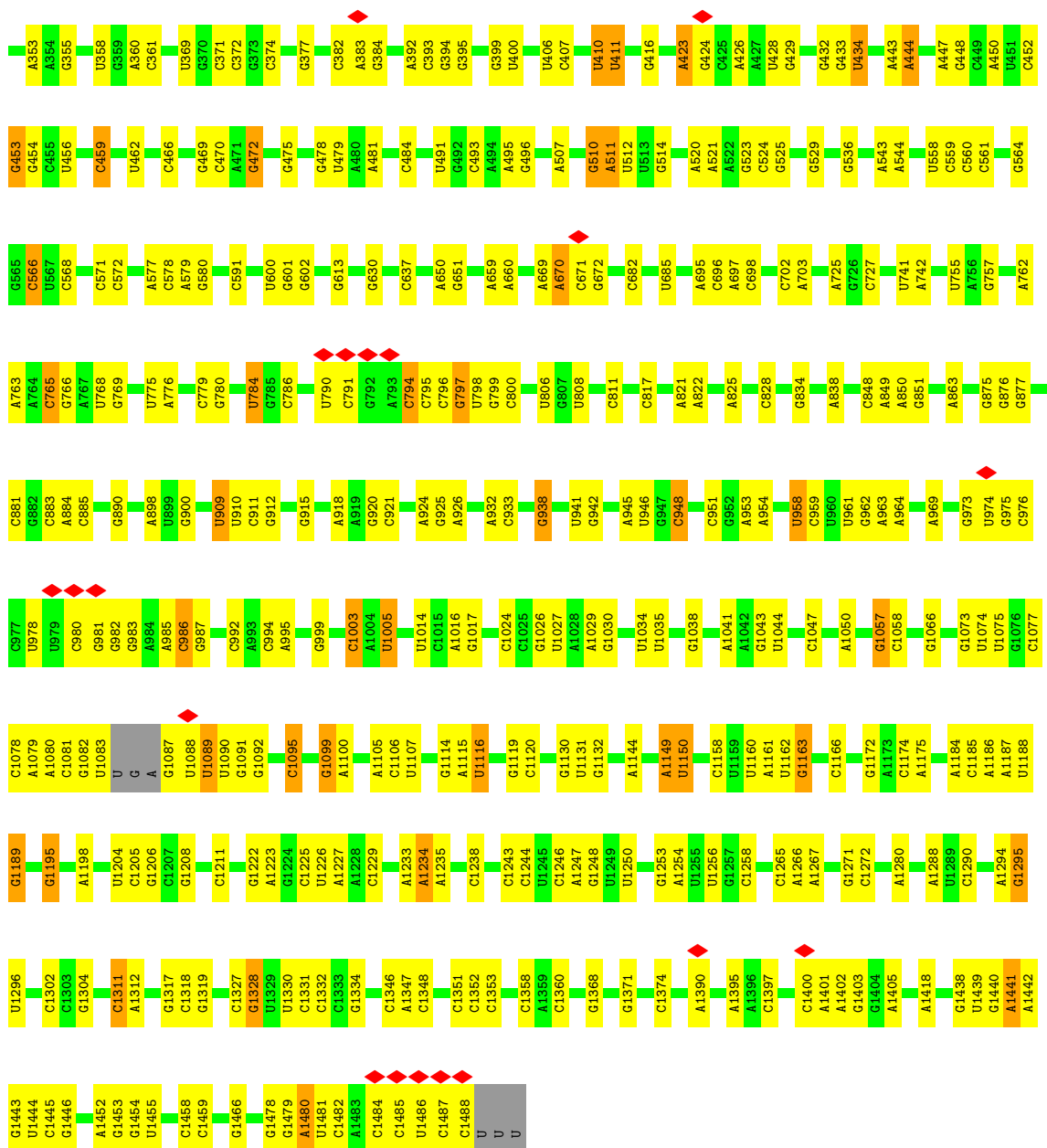


- Molecule 15: 30S ribosomal protein S18, chloroplastic

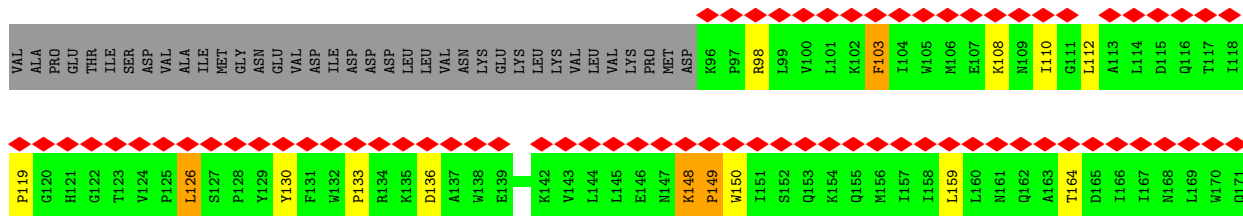


- Molecule 16: 30S ribosomal protein S19 alpha, chloroplastic





• Molecule 21: protein cS23



Chain d:



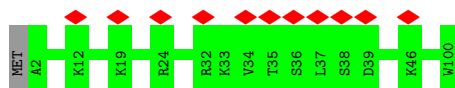
- Molecule 23: protein cS22

Chain v:



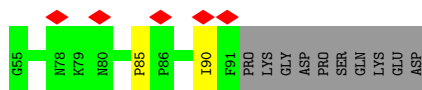
- Molecule 24: 30S ribosomal protein S14, chloroplastic

Chain n:



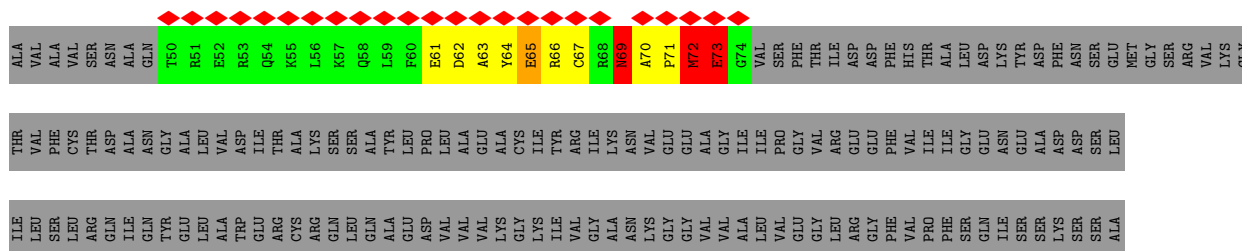
- Molecule 25: protein bTHXc

Chain x:



- Molecule 26: 30S ribosomal protein S1, chloroplastic

Chain 8:





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	81305	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.5	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	3700	Depositor
Magnification	133333	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.316	Depositor
Minimum map value	-0.172	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.05	Depositor
Map size (\AA)	403.19998, 403.19998, 403.19998	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.05, 1.05, 1.05	Depositor

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	b	0.75	8/1819 (0.4%)	0.96	8/2458 (0.3%)
2	c	0.48	0/1746	0.72	1/2348 (0.0%)
3	e	0.61	0/1307	0.77	2/1754 (0.1%)
4	f	0.44	0/904	0.69	0/1225
5	g	0.36	0/1175	0.62	0/1574
6	h	0.88	5/1103 (0.5%)	1.69	6/1477 (0.4%)
7	i	0.43	0/1038	0.70	0/1397
8	j	0.51	0/813	0.70	1/1099 (0.1%)
9	k	0.40	0/901	0.63	0/1214
10	l	0.62	0/983	0.80	4/1323 (0.3%)
11	m	0.45	0/909	0.75	2/1209 (0.2%)
12	o	0.42	0/532	0.65	0/707
13	p	0.52	0/674	0.71	0/902
14	q	0.50	0/647	0.64	0/867
15	r	0.49	0/522	0.76	2/697 (0.3%)
16	s	0.40	0/642	0.67	0/866
17	t	0.46	0/842	0.68	0/1127
18	u	1.10	3/396 (0.8%)	0.94	3/518 (0.6%)
19	y	0.45	0/852	0.70	0/1139
20	a	1.13	32/35582 (0.1%)	1.39	473/55510 (0.9%)
21	w	0.80	2/709 (0.3%)	1.23	11/965 (1.1%)
22	d	0.40	0/1661	0.72	2/2230 (0.1%)
23	v	1.49	16/1481 (1.1%)	1.24	13/1991 (0.7%)
24	n	0.37	0/835	0.62	0/1116
25	x	0.55	0/296	0.74	1/390 (0.3%)
26	8	0.87	5/1216 (0.4%)	1.61	28/1631 (1.7%)
All	All	0.97	71/59585 (0.1%)	1.24	557/87734 (0.6%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	b	0	2
2	c	0	3
3	e	0	1
4	f	0	1
5	g	0	1
7	i	0	2
8	j	0	1
10	l	0	3
11	m	0	2
18	u	0	1
21	w	0	7
22	d	0	2
23	v	0	15
26	8	0	17
All	All	0	58

The worst 5 of 71 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	v	142	PHE	CE1-CZ	-18.97	1.01	1.37
23	v	142	PHE	CE2-CZ	-17.85	1.03	1.37
23	v	142	PHE	CG-CD2	-15.89	1.15	1.38
6	h	67	ARG	CZ-NH2	-15.34	1.13	1.33
23	v	165	PHE	CE2-CZ	-14.94	1.08	1.37

The worst 5 of 557 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	h	67	ARG	NE-CZ-NH1	50.54	145.57	120.30
1	b	201	ASP	CB-CG-OD2	20.66	136.90	118.30
20	a	1440	G	N3-C2-N2	-20.49	105.56	119.90
20	a	7	G	C2-N3-C4	20.20	122.00	111.90
20	a	1441	A	N1-C2-N3	20.05	139.32	129.30

There are no chirality outliers.

5 of 58 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	b	168	VAL	Peptide
1	b	201	ASP	Sidechain
2	c	168	ILE	Peptide
2	c	86	GLU	Peptide

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Mol	Chain	Res	Type	Group
2	c	88	ARG	Peptide

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	b	1787	0	1828	0	0
2	c	1719	0	1807	0	0
3	e	1292	0	1355	0	0
4	f	886	0	888	0	0
5	g	1161	0	1237	0	0
6	h	1088	0	1149	0	0
7	i	1020	0	1072	0	0
8	j	796	0	841	0	0
9	k	887	0	933	0	0
10	l	967	0	1046	0	0
11	m	898	0	950	0	0
12	o	525	0	572	0	0
13	p	664	0	703	0	0
14	q	635	0	667	0	0
15	r	518	0	544	0	0
16	s	627	0	653	0	0
17	t	832	0	883	0	0
18	u	393	0	406	0	0
19	y	845	0	892	0	0
20	a	31777	0	16007	0	0
21	w	689	0	706	0	0
22	d	1633	0	1727	0	0
23	v	1464	0	1456	0	0
24	n	819	0	858	0	0
25	x	289	0	301	0	0
26	8	1201	0	1220	46	0
All	All	55412	0	40701	46	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 12.

The worst 5 of 46 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:8:317:HIS:HA	26:8:324:VAL:HA	1.47	0.94
26:8:291:GLN:HB3	26:8:327:SER:HA	1.60	0.83
26:8:342:PRO:HA	26:8:345:VAL:HB	1.61	0.83
26:8:63:ALA:O	26:8:66:ARG:C	2.22	0.78
26:8:365:ALA:O	26:8:366:MET:O	2.03	0.74

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	b	225/236 (95%)	195 (87%)	29 (13%)	1 (0%)	34	69
2	c	211/218 (97%)	181 (86%)	28 (13%)	2 (1%)	17	54
3	e	169/253 (67%)	150 (89%)	17 (10%)	2 (1%)	13	48
4	f	109/146 (75%)	85 (78%)	24 (22%)	0	100	100
5	g	147/155 (95%)	130 (88%)	16 (11%)	1 (1%)	22	59
6	h	132/134 (98%)	116 (88%)	16 (12%)	0	100	100
7	i	131/157 (83%)	107 (82%)	23 (18%)	1 (1%)	19	56
8	j	96/122 (79%)	83 (86%)	13 (14%)	0	100	100
9	k	116/138 (84%)	104 (90%)	12 (10%)	0	100	100
10	l	121/123 (98%)	100 (83%)	21 (17%)	0	100	100
11	m	108/126 (86%)	90 (83%)	18 (17%)	0	100	100
12	o	60/90 (67%)	59 (98%)	1 (2%)	0	100	100
13	p	78/88 (89%)	61 (78%)	17 (22%)	0	100	100
14	q	76/108 (70%)	64 (84%)	12 (16%)	0	100	100
15	r	62/101 (61%)	58 (94%)	4 (6%)	0	100	100
16	s	76/92 (83%)	61 (80%)	15 (20%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	t	103/108 (95%)	93 (90%)	10 (10%)	0	100	100
18	u	42/137 (31%)	39 (93%)	3 (7%)	0	100	100
19	y	106/236 (45%)	96 (91%)	10 (9%)	0	100	100
21	w	82/121 (68%)	79 (96%)	0	3 (4%)	3	28
22	d	197/201 (98%)	173 (88%)	22 (11%)	2 (1%)	15	51
23	v	188/198 (95%)	171 (91%)	14 (7%)	3 (2%)	9	43
24	n	97/100 (97%)	90 (93%)	7 (7%)	0	100	100
25	x	35/47 (74%)	30 (86%)	4 (11%)	1 (3%)	4	32
26	8	150/370 (40%)	116 (77%)	18 (12%)	16 (11%)	0	6
All	All	2917/3805 (77%)	2531 (87%)	354 (12%)	32 (1%)	18	50

5 of 32 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	e	148	ILE
21	w	149	PRO
23	v	105	MET
26	8	72	MET
26	8	73	GLU

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	b	192/201 (96%)	188 (98%)	4 (2%)	53	74
2	c	185/188 (98%)	185 (100%)	0	100	100
3	e	132/203 (65%)	128 (97%)	4 (3%)	41	66
4	f	98/125 (78%)	98 (100%)	0	100	100
5	g	120/126 (95%)	120 (100%)	0	100	100
6	h	117/117 (100%)	115 (98%)	2 (2%)	60	79
7	i	103/123 (84%)	102 (99%)	1 (1%)	76	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	j	90/110 (82%)	90 (100%)	0	100	100
9	k	92/109 (84%)	92 (100%)	0	100	100
10	l	106/106 (100%)	106 (100%)	0	100	100
11	m	97/109 (89%)	97 (100%)	0	100	100
12	o	58/85 (68%)	58 (100%)	0	100	100
13	p	71/79 (90%)	70 (99%)	1 (1%)	67	82
14	q	70/95 (74%)	70 (100%)	0	100	100
15	r	56/96 (58%)	56 (100%)	0	100	100
16	s	67/81 (83%)	67 (100%)	0	100	100
17	t	86/89 (97%)	84 (98%)	2 (2%)	50	71
18	u	40/118 (34%)	40 (100%)	0	100	100
19	y	97/213 (46%)	94 (97%)	3 (3%)	40	65
21	w	75/109 (69%)	74 (99%)	1 (1%)	69	83
22	d	178/180 (99%)	175 (98%)	3 (2%)	60	79
23	v	160/168 (95%)	158 (99%)	2 (1%)	69	83
24	n	89/90 (99%)	89 (100%)	0	100	100
25	x	28/37 (76%)	28 (100%)	0	100	100
26	8	129/310 (42%)	125 (97%)	4 (3%)	40	65
All	All	2536/3267 (78%)	2509 (99%)	27 (1%)	74	85

5 of 27 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
19	y	91	ARG
21	w	103	PHE
26	8	304	LEU
19	y	159	LEU
22	d	27	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 39 such sidechains are listed below:

Mol	Chain	Res	Type
22	d	57	HIS
23	v	196	ASN
22	d	112	ASN

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Mol	Chain	Res	Type
23	v	45	HIS
26	8	269	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
20	a	1477/1491 (99%)	310 (20%)	0

5 of 310 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
20	a	5	A
20	a	6	U
20	a	7	G
20	a	10	G
20	a	31	U

There are no RNA pucker outliers to report.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

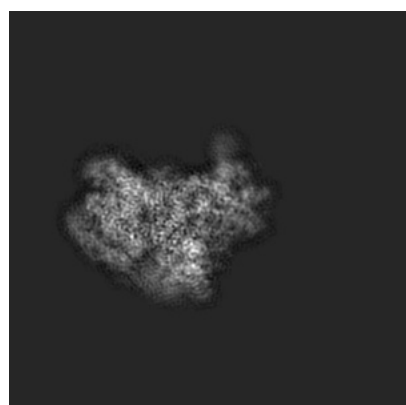
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6710. These allow visual inspection of the internal detail of the map and identification of artifacts.

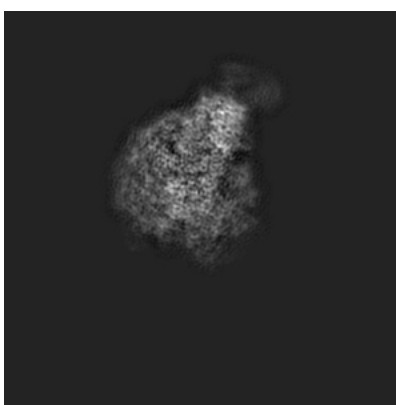
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

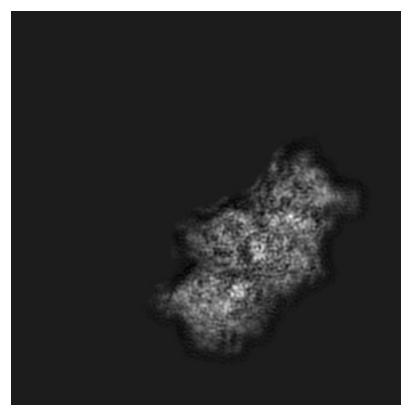
6.1.1 Primary map



X



Y

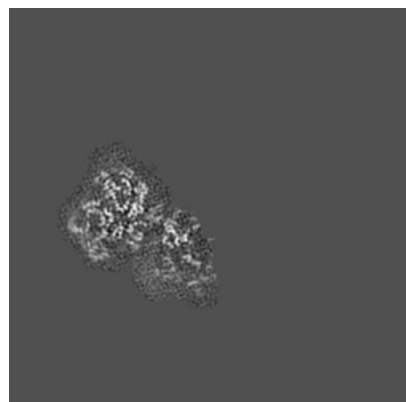


Z

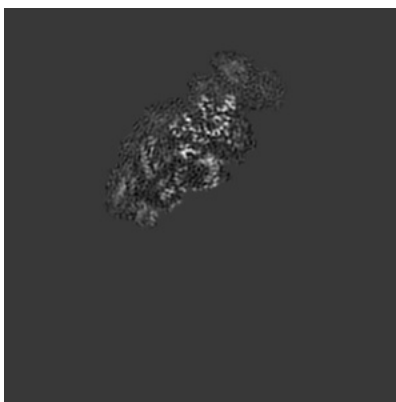
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

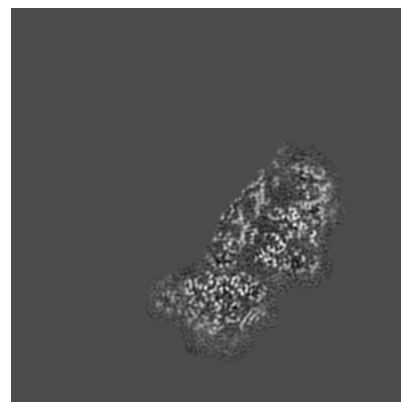
6.2.1 Primary map



X Index: 192



Y Index: 192

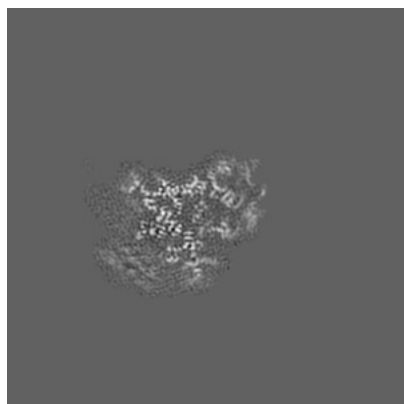


Z Index: 192

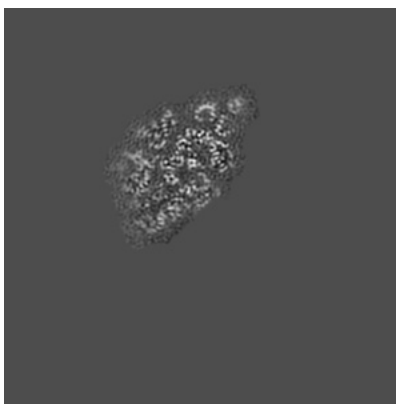
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

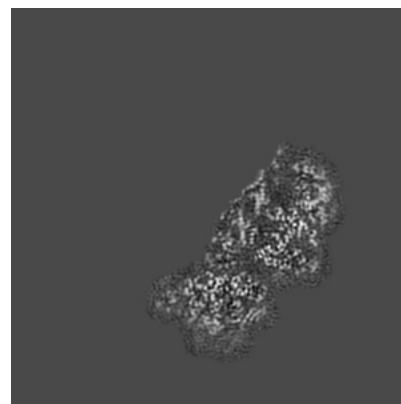
6.3.1 Primary map



X Index: 253



Y Index: 160



Z Index: 191

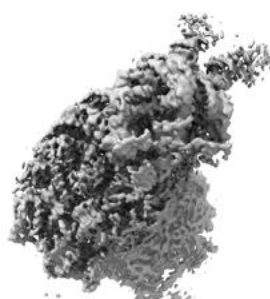
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

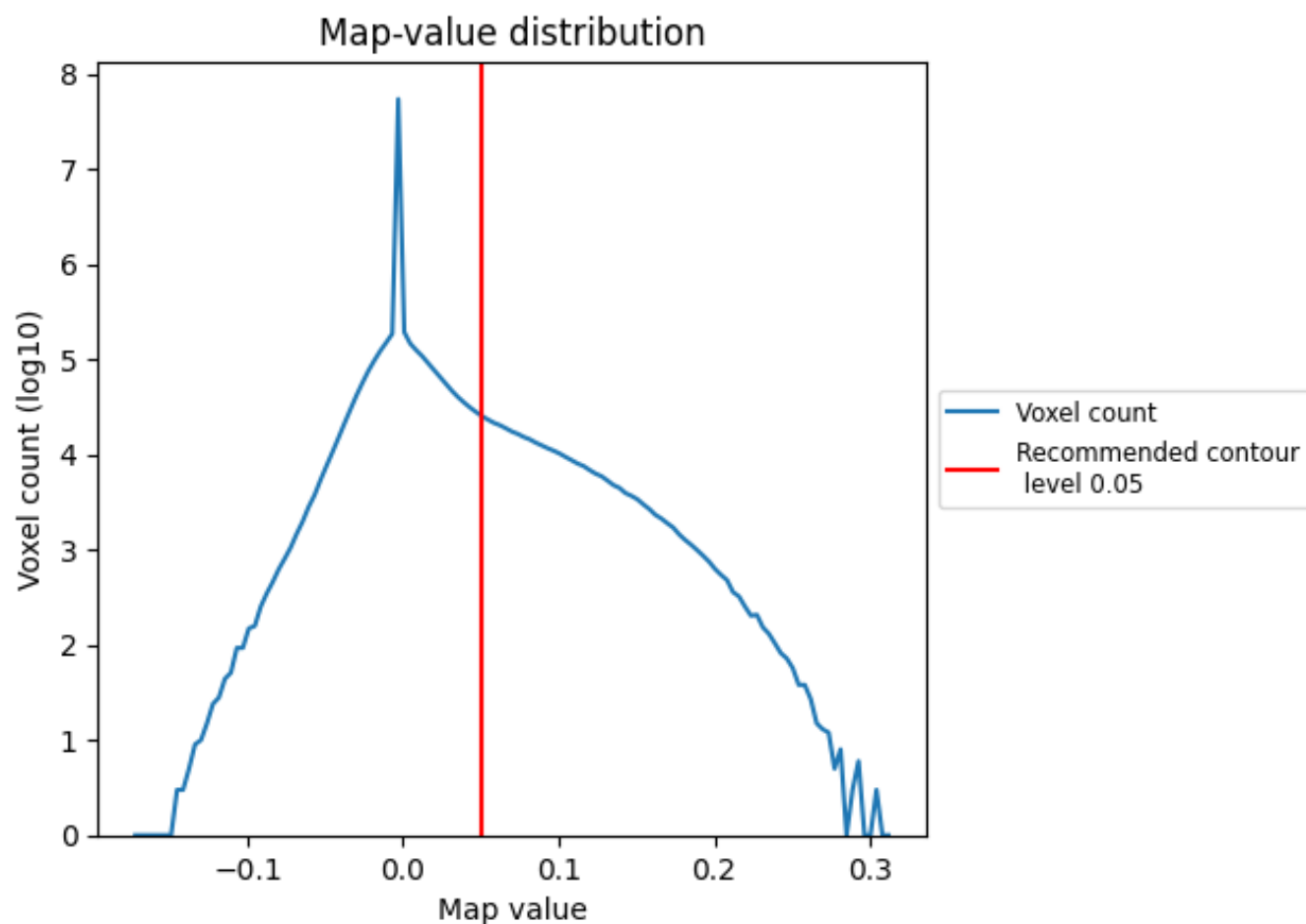
6.5 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

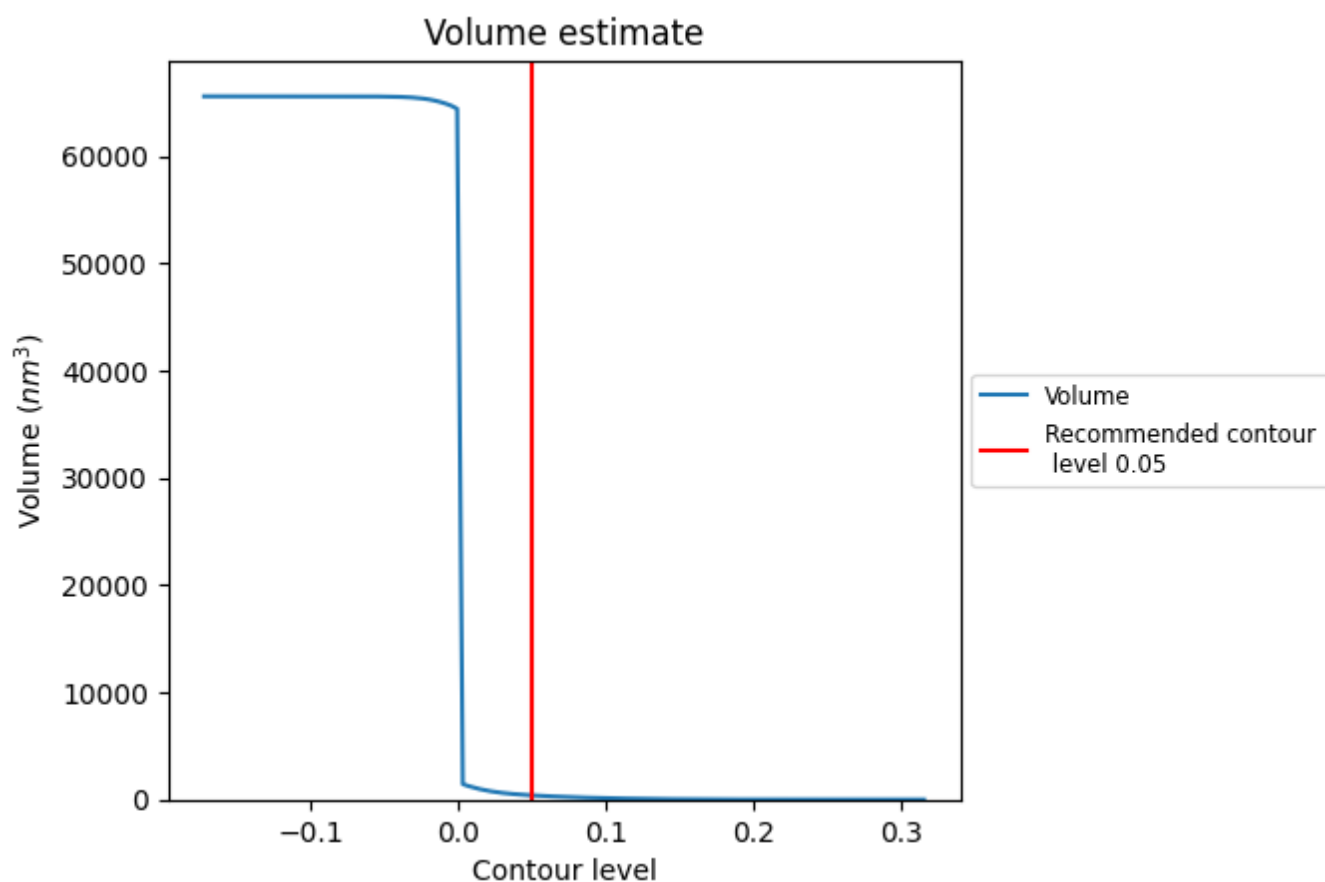
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

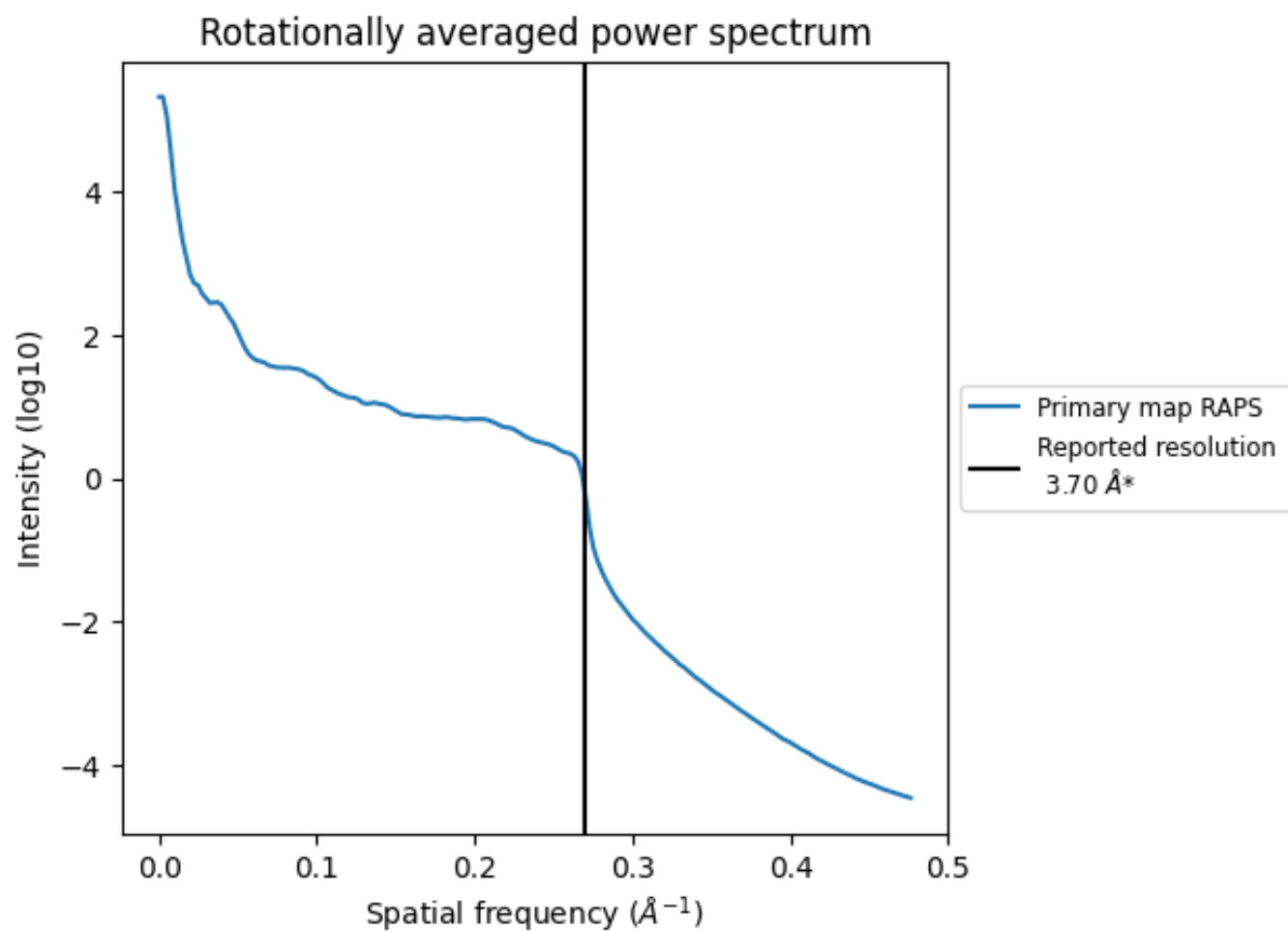
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 393 nm³; this corresponds to an approximate mass of 355 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

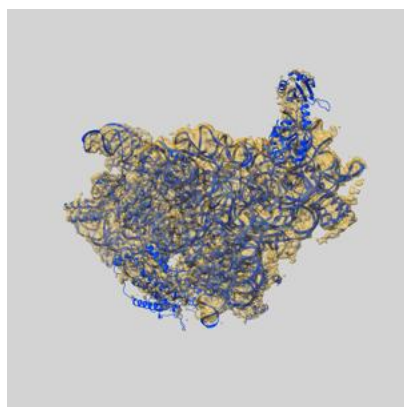
8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

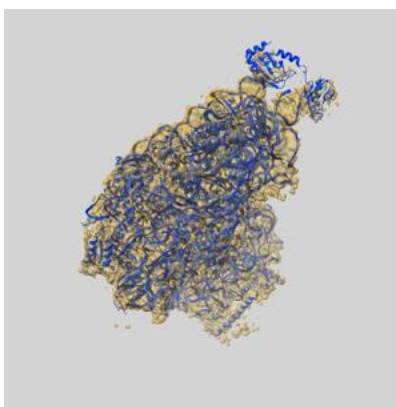
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-6710 and PDB model 5X8R. Per-residue inclusion information can be found in section [3](#) on page [8](#).

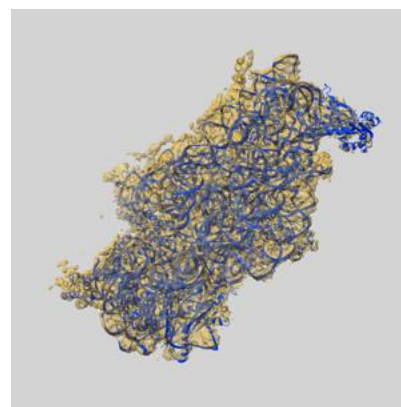
9.1 Map-model overlay [i](#)



X



Y



Z

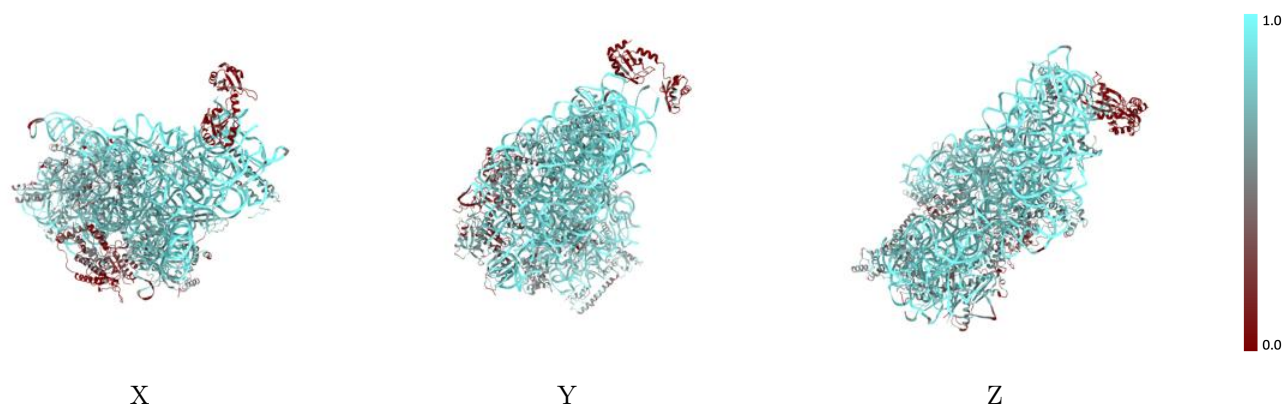
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



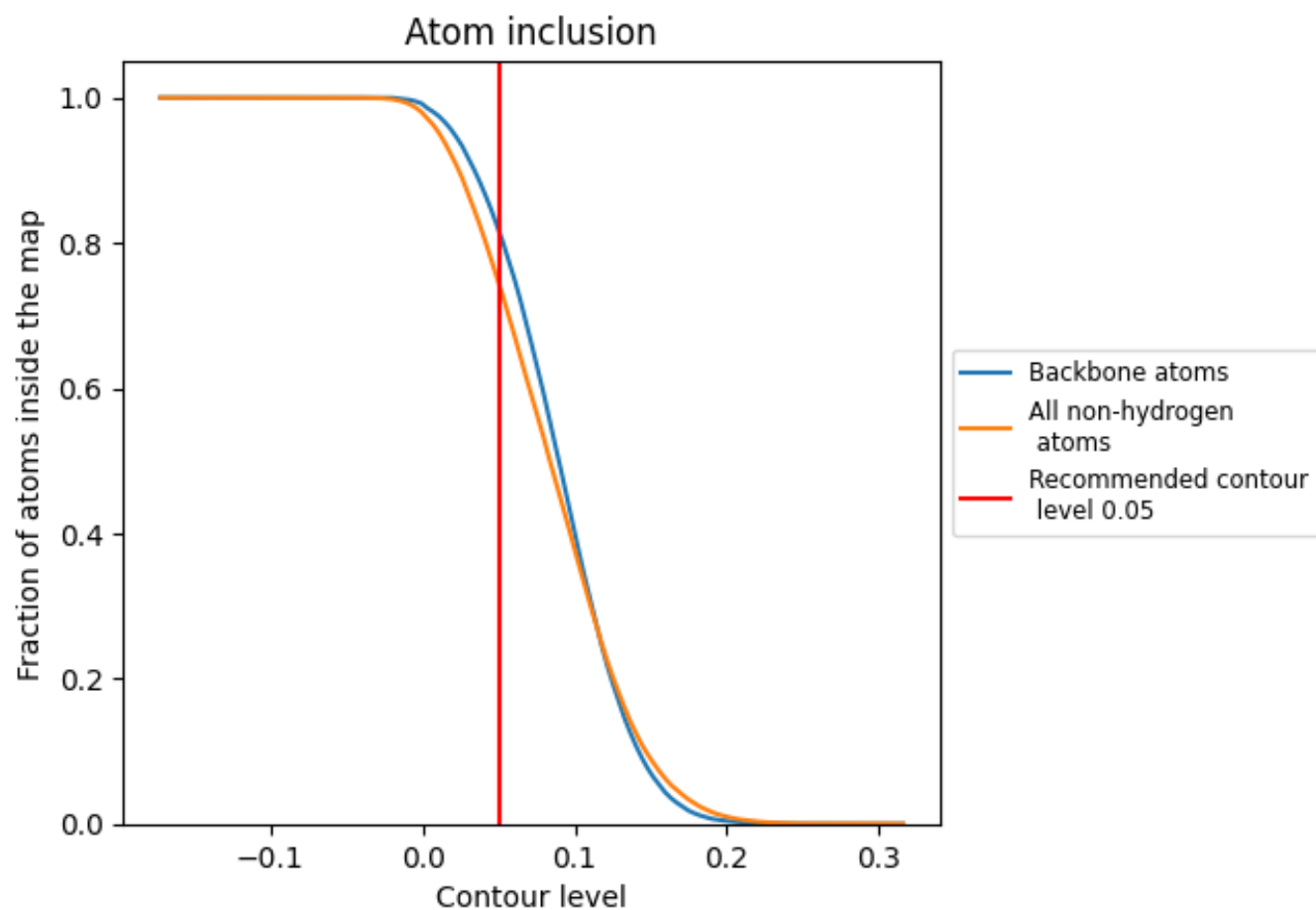
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.05).























































9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 75% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7463	 0.3930
8	 0.0281	 0.0120
a	 0.9009	 0.4330
b	 0.3429	 0.3270
c	 0.6462	 0.4160
d	 0.6607	 0.4040
e	 0.6894	 0.4310
f	 0.5410	 0.3560
g	 0.5164	 0.3730
h	 0.6784	 0.4220
i	 0.6851	 0.4000
j	 0.6208	 0.4020
k	 0.6332	 0.3940
l	 0.7068	 0.4640
m	 0.6104	 0.3210
n	 0.6467	 0.3870
o	 0.5354	 0.3860
p	 0.7281	 0.4350
q	 0.6893	 0.4520
r	 0.6287	 0.3840
s	 0.6504	 0.3850
t	 0.6513	 0.3400
u	 0.4919	 0.3180
v	 0.0848	 0.0540
w	 0.0619	 -0.0250
x	 0.6882	 0.4150
y	 0.5961	 0.4000

